

<!--StartFragment-->

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:00:21 ; Search time 199 Seconds
 (without alignments)
 1346.376 Million cell updates/sec

Title: US-10-716-359-16

Perfect score: 3104

Sequence: 1 MLYLENNAAQTQFSEPQYTNL.....FNFDMDARRNKQQRIKEEGE 586

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
1	3104	100.0	586	2	AAY05956			Aay05956 Human cel
2	3104	100.0	586	5	ABG95140			Abg95140 Human onc
3	3100	99.9	586	5	ABG95132			Abg95132 Human onc
4	3087	99.5	586	3	AAB11357			Aab11357 Human p63
5	3087	99.5	586	5	ABB74989			Abb74989 Human p53
6	3087	99.5	586	5	ABP61909			Abp61909 Human lun
7	3087	99.5	586	7	ADH36992			Adh36992 Human lun
8	3087	99.5	586	8	ADM56795			Adm56795 Human lun
9	3087	99.5	586	8	ADN04517			Adn04517 Antipsori
10	3087	99.5	586	9	ADU98487			Adu98487 Human p53
11	3087	99.5	586	9	AEB10295			Aeb10295 Cancer re
12	3087	99.5	586	9	AEE06149			Aee06149 p53 tumor
13	3080	99.2	586	2	AAY41032			Aay41032 Human lun
14	3080	99.2	586	3	AAB11317			Aab11317 Human lun
15	3080	99.2	586	5	ABB74949			Abb74949 Human lun

16	3080	99.2	586	5	ABP61869	Abp61869 Human lun
17	3080	99.2	586	7	ADE53447	Ade53447 Human lun
18	3080	99.2	586	7	ADH36806	Adh36806 Human lun
19	3080	99.2	586	8	ADM56609	Adm56609 Human lun
20	3080	99.2	586	8	ADN89653	Adn89653 Human lun
21	3080	99.2	586	9	ADU98301	Adu98301 Lung tumo
22	3080	99.2	586	9	AEB10109	Aeb10109 Cancer re
23	3080	99.2	586	9	AEE05963	Aee05963 Human lun
24	3078	99.2	586	7	ADA28428	Ada28428 p53 tumou
25	3077	99.1	586	7	ADA28242	Ada28242 Human lun
26	3066	98.8	586	2	AAY05962	Aay05962 Mouse cel
27	3033	97.7	641	2	AAY45247	Aay45247 Human p51
28	3033	97.7	641	2	AAY05953	Aay05953 Human cel
29	3033	97.7	641	4	AAB82129	Aab82129 Human pro
30	3033	97.7	641	5	ABG95142	Abg95142 Human onc
31	3033	97.7	687	7	ADL22695	Adl22695 Human dis
32	3029	97.6	641	3	AAB11358	Aab11358 Human p63
33	3029	97.6	641	5	ABG95136	Abg95136 Human onc
34	3029	97.6	641	5	ABG95128	Abg95128 Human onc
35	3029	97.6	641	5	ABB74990	Abb74990 Human p53
36	3029	97.6	641	5	ABP61910	Abp61910 Human lun
37	3029	97.6	641	7	ADA28429	Ada28429 p53 tumou
38	3029	97.6	641	7	ADH36993	Adh36993 Human lun
39	3029	97.6	641	8	ADM56796	Adm56796 Human lun
40	3029	97.6	641	9	ADU98488	Adu98488 Human p53
41	3029	97.6	641	9	AEB10296	Aeb10296 Cancer re
42	3029	97.6	641	9	AEE06150	Aee06150 p53 tumor
43	3025	97.5	680	3	AAY50997	Aay50997 Human KET
44	3025	97.5	680	3	AAB11361	Aab11361 Human p63
45	3025	97.5	680	5	ABB74993	Abb74993 Human p53
46	3025	97.5	680	5	ABP61913	Abp61913 Human lun
47	3025	97.5	680	7	ADA28432	Ada28432 p53 tumou
48	3025	97.5	680	7	ADH36996	Adh36996 Human lun
49	3025	97.5	680	8	ADM56799	Adm56799 Human lun
50	3025	97.5	680	8	ABM80526	Abm80526 Tumour-as
51	3025	97.5	680	8	ADU06284	Adu06284 Novel bro
52	3025	97.5	680	9	ADU98491	Adu98491 Human p53
53	3025	97.5	680	9	AEB10299	Aeb10299 Cancer re
54	3025	97.5	680	9	AEE06153	Aee06153 p53 tumor
55	2995	96.5	680	2	AAY05958	Aay05958 Human cel
56	2991	96.4	680	3	AAY50998	Aay50998 Rat KET p
57	2421	78.0	461	3	AAB11362	Aab11362 Human p63
58	2421	78.0	461	5	ABG95131	Abg95131 Human onc
59	2421	78.0	461	5	ABG95138	Abg95138 Human onc
60	2421	78.0	461	5	ABB74994	Abb74994 Human p53

<!--EndFragment-->

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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:01:02 ; Search time 306 Seconds
 (without alignments)
 1771.435 Million cell updates/sec

Title: US-10-716-359-16

Perfect score: 3104

Sequence: 1 MLYLENNAAQTQFSEPQYTNL..... FNFDMDARRNKQQRIKEEGE 586

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
1	3033	97.7	680	1	P73L_HUMAN			Q9h3d4 homo sapien
2	3026	97.5	582	2	Q3UVI3_MOUSE			Q3uvI3 mus musculu
3	3017	97.2	582	2	Q5CZX0_MOUSE			Q5czx0 mus musculu
4	2995	96.5	680	1	P73L_MOUSE			Q88898 mus musculu
5	2991	96.4	680	1	P73L_RAT			Q9jjp6 rattus norv
6	2962	95.4	582	2	Q9DEC7_CHICK			Q9dec7 gallus gall
7	2416	77.8	565	2	Q4S122_TETNG			Q4s122 tetraodon n
8	2344	75.5	576	2	Q8JFE3_BRARE			Q8jfe3 brachydanio
9	2330	75.1	588	2	Q8JHZ6_BRARE			Q8jhz6 brachydanio
10	1877	60.5	393	2	Q569E5_MOUSE			Q569e5 mus musculu
11	1826	58.8	457	2	Q8JHZ5_BRARE			Q8jhz5 brachydanio
12	1777	57.2	641	2	Q9W664_BARBU			Q9w664 barbus barb
13	1774	57.2	640	2	Q801Z7_BRARE			Q801z7 brachydanio
14	1771	57.1	640	2	Q6UNX2_BRARE			Q6unx2 brachydanio
15	1748.5	56.3	590	2	Q9JJP1_MOUSE			Q9jjp1 mus musculu
16	1744.5	56.2	631	2	Q9JJP2_MOUSE			Q9jjp2 mus musculu
17	1741	56.1	636	1	P73_HUMAN			O15350 homo sapien
18	1730.5	55.8	365	2	Q98SW0_XENLA			Q98sw0 xenopus lae
19	1720.5	55.4	637	1	P73_CERAE			Q9xsk8 cercopithec
20	1579	50.9	434	2	Q6DG24_BRARE			Q6dg24 brachydanio
21	1562	50.3	514	2	Q9CU77_MOUSE			Q9cu77 mus musculu
22	1507.5	48.6	494	2	Q3UT91_MOUSE			Q3ut91 mus musculu
23	1481	47.7	662	2	Q4S837_TETNG			Q4s837 tetraodon n

24	1464	47.2	555	2	Q5KQU6_BRARE	Q5kqu6 brachydanio
25	1459.5	47.0	497	2	Q9WUJ0_MOUSE	Q9wuj0 mus musculu
26	950.5	30.6	621	2	Q9NGC7_MYAAR	Q9ngc7 mya arenari
27	912	29.4	591	2	Q8T7V3_SPISO	Q8t7v3 spisula sol
28	912	29.4	596	2	Q6WG19_SPISO	Q6wg19 spisula sol
29	912	29.4	596	2	Q6WG20_SPISO	Q6wg20 spisula sol
30	896.5	28.9	564	2	Q27937_LOLFO	Q27937 loligo forb

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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:04:46 ; Search time 41 Seconds
 (without alignments)
 1375.196 Million cell updates/sec

Title: US-10-716-359-16

Perfect score: 3104

Sequence: 1 MLYLENNAAQTQFSEPQYTNL..... FNFDMDARRNKQQRIKEEGE 586

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : PIR_80:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	1774	57.2	640	2	JC7989	p73 protein - zebr
2	839.5	27.0	396	1	JH0631	cellular tumor ant
3	762	24.5	363	1	A29376	cellular tumor ant
4	758.5	24.4	367	1	S02193	cellular tumor ant
5	744	24.0	386	1	S51648	cellular tumor ant
6	723	23.3	391	1	S02192	cellular tumor ant
7	712	22.9	396	1	JH0633	cellular tumor ant
8	707.5	22.8	393	1	DNHU53	cellular tumor ant
9	703	22.6	393	1	S06594	cellular tumor ant
10	702	22.6	390	1	DNMS53	cellular tumor ant
11	700	22.6	391	2	JC6193	tumor suppressor p
12	697.5	22.5	393	2	JC6176	tumor suppressor p
13	688.5	22.2	381	2	S38824	cellular tumor ant
14	259.5	8.4	77	2	I46226	cellular tumor ant
15	152.5	4.9	925	2	T19361	hypothetical prote
16	134.5	4.3	901	2	JC6093	dead ringer nuclea
17	133	4.3	1081	2	S66736	transcription acti
18	133	4.3	1520	1	TVFFA	protein-tyrosine k
19	132.5	4.3	2578	2	A56922	transcription fact
20	130.5	4.2	2529	2	A56923	transcription fact
21	129	4.2	963	2	T40290	hypothetical prote

22	129	4.2	964	2	T41547	hypothetical prote
23	129	4.2	1051	2	G59436	KIAA1304 protein [
24	129	4.2	1621	2	T15264	hypothetical prote
25	128.5	4.1	628	2	S19150	hypothetical prote
26	126.5	4.1	628	2	JQ0110	hypothetical 69K p
27	126	4.1	2897	2	B48666	cell proliferation
28	126	4.1	3256	2	A48666	cell proliferation
29	125.5	4.0	628	2	S01955	hypothetical prote
30	125	4.0	724	2	T47149	hypothetical prote

<!--EndFragment-->

<!--StartFragment-->

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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:10:02 ; Search time 50 Seconds
 (without alignments)
 1025.859 Million cell updates/sec

Title: US-10-716-359-16

Perfect score: 3104

Sequence: 1 MLYLENNAAQTQFSEPQYTNL..... FNFDMDARRNKQQRIKEEGE 586

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : Issued_Patents_AA:*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PECTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB ID	
1	3104	100.0	586	2 US-09-538-106-16	Sequence 16, Appl
2	3104	100.0	586	3 US-09-529-583-16	Sequence 16, Appl
3	3087	99.5	586	2 US-09-643-597-338	Sequence 338, App
4	3087	99.5	586	2 US-09-542-615A-338	Sequence 338, App
5	3087	99.5	586	2 US-09-606-421B-338	Sequence 338, App
6	3087	99.5	586	2 US-09-630-940B-338	Sequence 338, App
7	3087	99.5	586	2 US-10-007-700-338	Sequence 338, App
8	3080	99.2	586	2 US-09-643-597-152	Sequence 152, App
9	3080	99.2	586	2 US-09-480-884A-152	Sequence 152, App
10	3080	99.2	586	2 US-09-542-615A-152	Sequence 152, App
11	3080	99.2	586	2 US-09-606-421B-152	Sequence 152, App
12	3080	99.2	586	2 US-09-221-107-152	Sequence 152, App
13	3080	99.2	586	2 US-09-466-396A-152	Sequence 152, App
14	3080	99.2	586	2 US-09-476-496A-152	Sequence 152, App
15	3080	99.2	586	2 US-09-630-940B-152	Sequence 152, App
16	3080	99.2	586	2 US-09-285-479-152	Sequence 152, App
17	3080	99.2	586	2 US-10-007-700-152	Sequence 152, App
18	3066	98.8	586	2 US-09-538-106-22	Sequence 22, Appl

19	3066	98.8	586	3	US-09-529-583-22	Sequence 22, Appl
20	3033	97.7	641	2	US-09-538-106-13	Sequence 13, Appl
21	3033	97.7	641	3	US-09-529-583-13	Sequence 13, Appl
22	3029	97.6	641	2	US-09-643-597-339	Sequence 339, App
23	3029	97.6	641	2	US-09-542-615A-339	Sequence 339, App
24	3029	97.6	641	2	US-09-606-421B-339	Sequence 339, App
25	3029	97.6	641	2	US-09-630-940B-339	Sequence 339, App
26	3029	97.6	641	2	US-10-007-700-339	Sequence 339, App
27	3025	97.5	680	2	US-09-643-597-342	Sequence 342, App
28	3025	97.5	680	2	US-09-542-615A-342	Sequence 342, App
29	3025	97.5	680	2	US-09-606-421B-342	Sequence 342, App
30	3025	97.5	680	2	US-09-630-940B-342	Sequence 342, App
31	3025	97.5	680	2	US-10-007-700-342	Sequence 342, App
32	2995	96.5	680	2	US-09-538-106-19	Sequence 19, Appl
33	2995	96.5	680	3	US-09-529-583-19	Sequence 19, Appl
34	2421	78.0	461	2	US-09-643-597-343	Sequence 343, App
35	2421	78.0	461	2	US-09-542-615A-343	Sequence 343, App
36	2421	78.0	461	2	US-09-606-421B-343	Sequence 343, App
37	2421	78.0	461	2	US-09-630-940B-343	Sequence 343, App
38	2421	78.0	461	2	US-09-538-106-17	Sequence 17, Appl
39	2421	78.0	461	2	US-10-007-700-343	Sequence 343, App
40	2421	78.0	461	3	US-09-529-583-17	Sequence 17, Appl
41	2398	77.3	461	2	US-09-538-106-23	Sequence 23, Appl
42	2398	77.3	461	3	US-09-529-583-23	Sequence 23, Appl
43	2350	75.7	516	2	US-09-643-597-344	Sequence 344, App
44	2350	75.7	516	2	US-09-542-615A-344	Sequence 344, App
45	2350	75.7	516	2	US-09-606-421B-344	Sequence 344, App
46	2350	75.7	516	2	US-09-630-940B-344	Sequence 344, App
47	2350	75.7	516	2	US-09-538-106-14	Sequence 14, Appl
48	2350	75.7	516	2	US-10-007-700-344	Sequence 344, App
49	2350	75.7	516	3	US-09-529-583-14	Sequence 14, Appl
50	2327	75.0	555	2	US-09-538-106-20	Sequence 20, Appl

<!--EndFragment-->

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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:21:46 ; Search time 186 Seconds
 (without alignments)
 1459.376 Million cell updates/sec

Title: US-10-716-359-16
 Perfect score: 3104
 Sequence: 1 MLYLENNAAQTQFSEPQYTNL.....FNFDMDARRNKQQRIKEEGE 586

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : Published_Applications_AA_Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	3104	100.0	586	4	US-10-716-359-16	Sequence 16, Appl
2	3104	100.0	586	5	US-10-469-469-306	Sequence 306, App
3	3104	100.0	586	6	US-11-109-831-16	Sequence 16, Appl
4	3100	99.9	586	5	US-10-469-469-290	Sequence 290, App
5	3087	99.5	586	3	US-09-735-705-338	Sequence 338, App
6	3087	99.5	586	3	US-09-850-716A-338	Sequence 338, App
7	3087	99.5	586	3	US-09-897-778-338	Sequence 338, App
8	3087	99.5	586	4	US-10-007-700-338	Sequence 338, App
9	3087	99.5	586	4	US-10-117-982-338	Sequence 338, App
10	3087	99.5	586	4	US-10-313-986-338	Sequence 338, App
11	3087	99.5	586	5	US-10-775-972-338	Sequence 338, App
12	3087	99.5	586	5	US-10-922-124-338	Sequence 338, App
13	3087	99.5	586	5	US-10-623-155-338	Sequence 338, App
14	3080	99.2	586	3	US-09-735-705-152	Sequence 152, App
15	3080	99.2	586	3	US-09-850-716A-152	Sequence 152, App
16	3080	99.2	586	3	US-09-897-778-152	Sequence 152, App
17	3080	99.2	586	3	US-09-466-396A-152	Sequence 152, App
18	3080	99.2	586	4	US-10-007-700-152	Sequence 152, App
19	3080	99.2	586	4	US-10-117-982-152	Sequence 152, App

20	3080	99.2	586	4	US-10-313-986-152	Sequence 152, App
21	3080	99.2	586	5	US-10-775-972-152	Sequence 152, App
22	3080	99.2	586	5	US-10-922-124-152	Sequence 152, App
23	3080	99.2	586	5	US-10-623-155-152	Sequence 152, App
24	3066	98.8	586	4	US-10-716-359-22	Sequence 22, Appl
25	3066	98.8	586	6	US-11-109-831-22	Sequence 22, Appl
26	3033	97.7	641	4	US-10-716-359-13	Sequence 13, Appl
27	3033	97.7	641	5	US-10-469-469-310	Sequence 310, App
28	3033	97.7	641	6	US-11-109-831-13	Sequence 13, Appl
29	3029	97.6	641	3	US-09-735-705-339	Sequence 339, App
30	3029	97.6	641	3	US-09-850-716A-339	Sequence 339, App
31	3029	97.6	641	3	US-09-897-778-339	Sequence 339, App
32	3029	97.6	641	4	US-10-007-700-339	Sequence 339, App
33	3029	97.6	641	4	US-10-117-982-339	Sequence 339, App
34	3029	97.6	641	4	US-10-313-986-339	Sequence 339, App
35	3029	97.6	641	5	US-10-775-972-339	Sequence 339, App
36	3029	97.6	641	5	US-10-922-124-339	Sequence 339, App
37	3029	97.6	641	5	US-10-623-155-339	Sequence 339, App
38	3029	97.6	641	5	US-10-469-469-282	Sequence 282, App
39	3029	97.6	641	5	US-10-469-469-298	Sequence 298, App
40	3025	97.5	680	3	US-09-735-705-342	Sequence 342, App
41	3025	97.5	680	3	US-09-850-716A-342	Sequence 342, App
42	3025	97.5	680	3	US-09-897-778-342	Sequence 342, App
43	3025	97.5	680	4	US-10-007-700-342	Sequence 342, App
44	3025	97.5	680	4	US-10-117-982-342	Sequence 342, App
45	3025	97.5	680	4	US-10-313-986-342	Sequence 342, App
46	3025	97.5	680	5	US-10-775-972-342	Sequence 342, App
47	3025	97.5	680	5	US-10-922-124-342	Sequence 342, App
48	3025	97.5	680	5	US-10-623-155-342	Sequence 342, App
49	2995	96.5	680	4	US-10-716-359-19	Sequence 19, Appl
50	2995	96.5	680	6	US-11-109-831-19	Sequence 19, Appl
51	2421	78.0	461	3	US-09-735-705-343	Sequence 343, App
52	2421	78.0	461	3	US-09-850-716A-343	Sequence 343, App
53	2421	78.0	461	3	US-09-897-778-343	Sequence 343, App
54	2421	78.0	461	4	US-10-007-700-343	Sequence 343, App
55	2421	78.0	461	4	US-10-117-982-343	Sequence 343, App
56	2421	78.0	461	4	US-10-313-986-343	Sequence 343, App
57	2421	78.0	461	4	US-10-716-359-17	Sequence 17, Appl
58	2421	78.0	461	5	US-10-775-972-343	Sequence 343, App
59	2421	78.0	461	5	US-10-922-124-343	Sequence 343, App
60	2421	78.0	461	5	US-10-623-155-343	Sequence 343, App

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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:23:46 ; Search time 46 Seconds
 (without alignments)
 1246.430 Million cell updates/sec

Title: US-10-716-359-16
 Perfect score: 3104
 Sequence: 1 MLYLENNAAQTQFSEPQYTNL..... FNFDMDARRNKQQRIKEEGE 586

Scoring table: BLOSUM62
 Gapext 0.5 , Gapext 0.5

Searched: 390055 seqs, 97842647 residues

Total number of hits satisfying chosen parameters: 390055

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : Published_Applications_AA_New:
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB	ID
<hr/>					
1	3033	97.7	641	7	US-11-340-715-4
2	2995	96.5	641	7	US-11-340-715-11
3	1813	58.4	448	7	US-11-340-715-1
4	1746	56.2	587	6	US-10-489-730-2
5	1741	56.1	636	7	US-11-340-715-8
6	1718.5	55.4	661	6	US-10-489-730-11
7	1420.5	45.8	450	6	US-10-489-730-4
8	1415.5	45.6	499	7	US-11-340-715-6
9	1256	40.5	426	6	US-10-489-730-6
10	1046	33.7	312	7	US-11-340-715-7
11	960.5	30.9	349	7	US-11-340-715-9
12	707.5	22.8	354	6	US-10-538-066-763
13	707.5	22.8	393	6	US-10-538-066-367
14	707.5	22.8	393	7	US-11-315-777-9
15	707.5	22.8	393	7	US-11-340-715-3
16	707.5	22.8	393	7	US-11-009-357-6
17	707.5	22.8	393	7	US-11-319-873-9

18	707.5	22.8	393	7	US-11-254-926-9	Sequence 9, Appli
19	707.5	22.8	393	7	US-11-304-280-9	Sequence 9, Appli
20	707.5	22.8	393	7	US-11-239-548-9	Sequence 9, Appli
21	707.5	22.8	425	7	US-11-009-357-2	Sequence 2, Appli
22	702.5	22.6	393	6	US-10-546-829-1	Sequence 1, Appli
23	702.5	22.6	393	7	US-11-404-146-3	Sequence 3, Appli
24	699.5	22.5	393	7	US-11-371-354-72585	Sequence 72585, A
25	316	10.2	102	6	US-10-538-066-765	Sequence 765, App
26	291.5	9.4	100	6	US-10-489-730-12	Sequence 12, Appl
27	285.5	9.2	100	6	US-10-489-730-14	Sequence 14, Appl
28	284.5	9.2	100	6	US-10-489-730-13	Sequence 13, Appl
29	133	4.3	2801	7	US-11-375-359-120	Sequence 120, App
30	133	4.3	2896	7	US-11-375-359-121	Sequence 121, App

<!--StartFragment-->

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 27, 2006, 19:24:15 ; Search time 59 Seconds
 (without alignments)
 4094.024 Million cell updates/sec

Title: US-10-716-359-4

Perfect score: 3260

Sequence: 1 atgttgtacctggaaaacaa.....tcaaagaggagggggagtga 1761

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 5179358

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```

-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10716359/runat_27122006_140406_325/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10716359@CGN_1_1_440@runat_27122006_140406_325 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				
No.	Score	Match	Length	DB	ID

Description

1	3104	95.2	586	2	AAY05956	Aay05956 Human cel
2	3104	95.2	586	5	ABG95140	Abg95140 Human onc
3	3100	95.1	586	5	ABG95132	Abg95132 Human onc
4	3087	94.7	586	3	AAB11357	Aab11357 Human p63
5	3087	94.7	586	5	ABB74989	Abb74989 Human p53
6	3087	94.7	586	5	ABP61909	Abp61909 Human lun
7	3087	94.7	586	7	ADH36992	Adh36992 Human lun
8	3087	94.7	586	8	ADM56795	Adm56795 Human lun
9	3087	94.7	586	8	ADN04517	Adn04517 Antipsori
10	3087	94.7	586	9	ADU98487	Adu98487 Human p53
11	3087	94.7	586	9	AEB10295	Aeb10295 Cancer re
12	3087	94.7	586	9	AEE06149	Aee06149 p53 tumor
13	3080	94.5	586	2	AAY41032	Aay41032 Human lun
14	3080	94.5	586	3	AAB11317	Aab11317 Human lun
15	3080	94.5	586	5	ABB74949	Abb74949 Human lun
16	3080	94.5	586	5	ABP61869	Abp61869 Human lun
17	3080	94.5	586	7	ADE53447	Ade53447 Human lun
18	3080	94.5	586	7	ADH36806	Adh36806 Human lun
19	3080	94.5	586	8	ADM56609	Adm56609 Human lun
20	3080	94.5	586	8	ADN89653	Adn89653 Human lun
21	3080	94.5	586	9	ADU98301	Adu98301 Lung tumo
22	3080	94.5	586	9	AEB10109	Aeb10109 Cancer re
23	3080	94.5	586	9	AEE05963	Aee05963 Human lun
24	3078	94.4	586	7	ADA28428	Ada28428 p53 tumou
25	3077	94.4	586	7	ADA28242	Ada28242 Human lun
26	3066	94.0	586	2	AAY05962	Aay05962 Mouse cel
27	3033	93.0	641	2	AAY45247	Aay45247 Human p51
28	3033	93.0	641	2	AAY05953	Aay05953 Human cel
29	3033	93.0	641	4	AAB82129	Aab82129 Human pro
30	3033	93.0	641	5	ABG95142	Abg95142 Human onc
31	3033	93.0	687	7	ADL22695	Adl22695 Human dis
32	3029	92.9	641	3	AAB11358	Aab11358 Human p63
33	3029	92.9	641	5	ABG95136	Abg95136 Human onc
34	3029	92.9	641	5	ABG95128	Abg95128 Human onc
35	3029	92.9	641	5	ABB74990	Abb74990 Human p53
36	3029	92.9	641	5	ABP61910	Abp61910 Human lun
37	3029	92.9	641	7	ADA28429	Ada28429 p53 tumou
38	3029	92.9	641	7	ADH36993	Adh36993 Human lun
39	3029	92.9	641	8	ADM56796	Adm56796 Human lun
40	3029	92.9	641	9	ADU98488	Adu98488 Human p53
41	3029	92.9	641	9	AEB10296	Aeb10296 Cancer re
42	3029	92.9	641	9	AEE06150	Aee06150 p53 tumor
43	3025	92.8	680	3	AAY50997	Aay50997 Human KET
44	3025	92.8	680	3	AAB11361	Aab11361 Human p63
45	3025	92.8	680	5	ABB74993	Abb74993 Human p53

<!--EndFragment-->

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 27, 2006, 19:26:20 ; Search time 107.5 Seconds
 (without alignments)
 4545.914 Million cell updates/sec

Title: US-10-716-359-4

Perfect score: 3260

Sequence: 1 atgttgtacctggaaaacaa.....tcaaagaggaggggagtga 1761

Scoring table: BLOSUM62

Xgapop	10.0	, Xgapext	0.5
Ygapop	10.0	, Ygapext	0.5
Fgapop	6.0	, Fgapext	7.0
Delop	6.0	, Delext	7.0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10716359/runat_27122006_140407_336/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10716359_@CGN_1_1_891_@runat_27122006_140407_336 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	3033	93.0	680	1	P73L_HUMAN	Q9h3d4 homo sapien
2	3026	92.8	582	2	Q3UVI3_MOUSE	Q3uvic3 mus musculu
3	3017	92.5	582	2	Q5CZX0_MOUSE	Q5czx0 mus musculu
4	2995	91.9	680	1	P73L_MOUSE	Q88898 mus musculu
5	2991	91.7	680	1	P73L_RAT	Q9jjp6 rattus norv
6	2962	90.9	582	2	Q9DEC7_CHICK	Q9dec7 gallus gall
7	2416	74.1	565	2	Q4S122_TETNG	Q4s122 tetraodon n
8	2344	71.9	576	2	Q8JFE3_BRARE	Q8jfe3 brachydanio

9	2330	71.5	588	2	Q8JHZ6_BRARE	Q8jhz6 brachydanio
10	1877	57.6	393	2	Q569E5_MOUSE	Q569e5 mus musculu
11	1826	56.0	457	2	Q8JHZ5_BRARE	Q8jhz5 brachydanio
12	1777	54.5	641	2	Q9W664_BARBU	Q9w664 barbus barb
13	1774	54.4	640	2	Q801Z7_BRARE	Q801z7 brachydanio
14	1771	54.3	640	2	Q6UNX2_BRARE	Q6unx2 brachydanio
15	1748.5	53.6	590	2	Q9JJP1_MOUSE	Q9jjp1 mus musculu
16	1744.5	53.5	631	2	Q9JJP2_MOUSE	Q9jjp2 mus musculu
17	1741	53.4	636	1	P73_HUMAN	Q15350 homo sapien
18	1730.5	53.1	365	2	Q98SW0_XENLA	Q98sw0 xenopus lae
19	1720.5	52.8	637	1	P73_CERAE	Q9xsk8 cercopithec
20	1649.5	50.6	434	2	Q6DG24_BRARE	Q6dg24 brachydanio
21	1562	47.9	514	2	Q9CU77_MOUSE	Q9cu77 mus musculu
22	1507.5	46.2	494	2	Q3UT91_MOUSE	Q3ut91 mus musculu
23	1481	45.4	662	2	Q4S837_TETNG	Q4s837 tetraodon n
24	1464	44.9	555	2	Q5KQU6_BRARE	Q5kqu6 brachydanio
25	1459.5	44.8	497	2	Q9WUJ0_MOUSE	Q9wuj0 mus musculu
26	950.5	29.2	621	2	Q9NGC7_MYAAR	Q9ngc7 mya arenari
27	912	28.0	591	2	Q8T7V3_SPISO	Q8t7v3 spisula sol
28	912	28.0	596	2	Q6WG19_SPISO	Q6wg19 spisula sol
29	912	28.0	596	2	Q6WG20_SPISO	Q6wg20 spisula sol
30	898.5	27.6	564	2	Q27937_LOLFO	Q27937 loligo forb

<!--StartFragment-->

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 27, 2006, 19:36:35 ; Search time 13.3 Seconds
 (without alignments)
 3821.903 Million cell updates/sec

Title: US-10-716-359-4

Perfect score: 3260

Sequence: 1 atgttgtacctggaaaacaa.....tcaaagaggagggggagtga 1761

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```

-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10716359/runat_27122006_140410_379/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10716359_@CGN_1_1_92_@runat_27122006_140410_379 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
<hr/>								
1	1774	54.4	640	2	JC7989			p73 protein - zebr
2	839.5	25.8	396	1	JH0631			cellular tumor ant
3	773.5	23.7	367	1	S02193			cellular tumor ant
4	762	23.4	363	1	A29376			cellular tumor ant
5	747.5	22.9	386	1	S51648			cellular tumor ant
6	736.5	22.6	391	1	S02192			cellular tumor ant

7	726	22.3	393	1	DNHU53	cellular tumor ant
8	719.5	22.1	393	1	S06594	cellular tumor ant
9	712	21.8	396	1	JH0633	cellular tumor ant
10	709.5	21.8	390	1	DNMS53	cellular tumor ant
11	701.5	21.5	391	2	JC6193	tumor suppressor p
12	697.5	21.4	393	2	JC6176	tumor suppressor p
13	692.5	21.2	381	2	S38824	cellular tumor ant
14	259.5	8.0	77	2	I46226	cellular tumor ant
15	161	4.9	925	2	T19361	hypothetical prote
16	152.5	4.7	3570	2	T45025	mucin MUC5B, trach
17	151.5	4.6	3020	2	A43932	mucin 2 precursor,
18	151	4.6	2715	2	T13049	eyelid - fruit fly
19	150	4.6	1006	2	T42731	atrophin-1 related
20	150	4.6	1188	2	S49915	extensin-like prot
21	147.5	4.5	620	2	S06733	hydroxyproline-ric
22	144.5	4.4	862	2	B53689	homeotic protein C
23	142.5	4.4	2359	2	T03094	A-kinase anchor pr
24	140.5	4.3	1199	2	A40670	nuclear envelope p
25	140.5	4.3	2232	2	T34434	hypothetical prote
26	140	4.3	847	2	F96531	hypothetical prote
27	139	4.3	1285	2	T14171	ataxin-2 - mouse
28	139	4.3	1613	2	S39059	protein BRG1 - hum
29	138	4.2	1510	2	T33100	hypothetical prote
30	136	4.2	400	2	S58222	PQ-rich protein -
31	136	4.2	650	2	T04487	hypothetical prote
32	135.5	4.2	891	2	G84693	probable proline-r
33	135.5	4.2	2649	2	T51023	hypothetical prote
34	135	4.1	975	2	S33121	homeotic protein C
35	135	4.1	1240	2	JC5209	insulin receptor s
36	135	4.1	1242	2	JS0670	insulin receptor s
37	134.5	4.1	628	2	JQ0110	hypothetical 69K p
38	134.5	4.1	901	2	JC6093	dead ringer nuclea
39	134	4.1	1520	1	TVFFA	protein-tyrosine k
40	134	4.1	1791	2	T24089	hypothetical prote
41	133.5	4.1	477	2	T46304	hypothetical prote
42	133.5	4.1	964	2	T41547	hypothetical prote
43	133	4.1	817	2	S51342	verprolin - yeast
44	133	4.1	1054	2	T43226	translation initia
45	133	4.1	1081	2	S66736	transcription acti

<!--EndFragment-->

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 27, 2006, 19:54:31 ; Search time 12.8 Seconds
 (without alignments)
 3612.690 Million cell updates/sec

Title: US-10-716-359-4
 Perfect score: 3260
 Sequence: 1 atgttgtacctggaaaacaa.....tcaaagaggagggggagtga 1761

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 1301182

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp
 -Q=/abss/ABSSWEB_spool/US10716359/runat_27122006_140412_434/app_query.fasta_1
 -DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
 -LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -HOST=abss02p -USER=US10716359_@CGN_1_1_84_@runat_27122006_140412_434 -NCPU=6
 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PECTUS_COMB.pep:
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB	
1	3104	95.2	586	2	US-09-538-106-16 Sequence 16, Appl
2	3104	95.2	586	3	US-09-529-583-16 Sequence 16, Appl
3	3087	94.7	586	2	US-09-643-597-338 Sequence 338, App

4	3087	94.7	586	2	US-09-542-615A-338	Sequence 338, App
5	3087	94.7	586	2	US-09-606-421B-338	Sequence 338, App
6	3087	94.7	586	2	US-09-630-940B-338	Sequence 338, App
7	3087	94.7	586	2	US-10-007-700-338	Sequence 338, App
8	3080	94.5	586	2	US-09-643-597-152	Sequence 152, App
9	3080	94.5	586	2	US-09-480-884A-152	Sequence 152, App
10	3080	94.5	586	2	US-09-542-615A-152	Sequence 152, App
11	3080	94.5	586	2	US-09-606-421B-152	Sequence 152, App
12	3080	94.5	586	2	US-09-221-107-152	Sequence 152, App
13	3080	94.5	586	2	US-09-466-396A-152	Sequence 152, App
14	3080	94.5	586	2	US-09-476-496A-152	Sequence 152, App
15	3080	94.5	586	2	US-09-630-940B-152	Sequence 152, App
16	3080	94.5	586	2	US-09-285-479-152	Sequence 152, App
17	3080	94.5	586	2	US-10-007-700-152	Sequence 152, App
18	3066	94.0	586	2	US-09-538-106-22	Sequence 22, Appl
19	3066	94.0	586	3	US-09-529-583-22	Sequence 22, Appl
20	3033	93.0	641	2	US-09-538-106-13	Sequence 13, Appl
21	3033	93.0	641	3	US-09-529-583-13	Sequence 13, Appl
22	3029	92.9	641	2	US-09-643-597-339	Sequence 339, App
23	3029	92.9	641	2	US-09-542-615A-339	Sequence 339, App
24	3029	92.9	641	2	US-09-606-421B-339	Sequence 339, App
25	3029	92.9	641	2	US-09-630-940B-339	Sequence 339, App
26	3029	92.9	641	2	US-10-007-700-339	Sequence 339, App
27	3025	92.8	680	2	US-09-643-597-342	Sequence 342, App
28	3025	92.8	680	2	US-09-542-615A-342	Sequence 342, App
29	3025	92.8	680	2	US-09-606-421B-342	Sequence 342, App
30	3025	92.8	680	2	US-09-630-940B-342	Sequence 342, App
31	3025	92.8	680	2	US-10-007-700-342	Sequence 342, App
32	2995	91.9	680	2	US-09-538-106-19	Sequence 19, Appl
33	2995	91.9	680	3	US-09-529-583-19	Sequence 19, Appl
34	2421	74.3	461	2	US-09-643-597-343	Sequence 343, App
35	2421	74.3	461	2	US-09-542-615A-343	Sequence 343, App
36	2421	74.3	461	2	US-09-606-421B-343	Sequence 343, App
37	2421	74.3	461	2	US-09-630-940B-343	Sequence 343, App
38	2421	74.3	461	2	US-09-538-106-17	Sequence 17, Appl
39	2421	74.3	461	2	US-10-007-700-343	Sequence 343, App
40	2421	74.3	461	3	US-09-529-583-17	Sequence 17, Appl
41	2398	73.6	461	2	US-09-538-106-23	Sequence 23, Appl
42	2398	73.6	461	3	US-09-529-583-23	Sequence 23, Appl
43	2350	72.1	516	2	US-09-643-597-344	Sequence 344, App
44	2350	72.1	516	2	US-09-542-615A-344	Sequence 344, App
45	2350	72.1	516	2	US-09-606-421B-344	Sequence 344, App

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 27, 2006, 20:28:36 ; Search time 58.9 Seconds
 (without alignments)
 4154.778 Million cell updates/sec

Title: US-10-716-359-4
 Perfect score: 3260
 Sequence: 1 atgttgtacctggaaaacaa.....tcaaagaggagggggagtga 1761

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 4195594

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10716359/runat_27122006_140422_629/app_query.fasta_1
-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10716359@CGN_1_1_446@runat_27122006_140422_629 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Published_Applications_AA_Main:*
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	3104	95.2	586	4	US-10-716-359-16	Sequence 16, Appl
2	3104	95.2	586	5	US-10-469-469-306	Sequence 306, App
3	3104	95.2	586	6	US-11-109-831-16	Sequence 16, Appl

4	3100	95.1	586	5	US-10-469-469-290	Sequence 290, App
5	3087	94.7	586	3	US-09-735-705-338	Sequence 338, App
6	3087	94.7	586	3	US-09-850-716A-338	Sequence 338, App
7	3087	94.7	586	3	US-09-897-778-338	Sequence 338, App
8	3087	94.7	586	4	US-10-007-700-338	Sequence 338, App
9	3087	94.7	586	4	US-10-117-982-338	Sequence 338, App
10	3087	94.7	586	4	US-10-313-986-338	Sequence 338, App
11	3087	94.7	586	5	US-10-775-972-338	Sequence 338, App
12	3087	94.7	586	5	US-10-922-124-338	Sequence 338, App
13	3087	94.7	586	5	US-10-623-155-338	Sequence 338, App
14	3080	94.5	586	3	US-09-735-705-152	Sequence 152, App
15	3080	94.5	586	3	US-09-850-716A-152	Sequence 152, App
16	3080	94.5	586	3	US-09-897-778-152	Sequence 152, App
17	3080	94.5	586	3	US-09-466-396A-152	Sequence 152, App
18	3080	94.5	586	4	US-10-007-700-152	Sequence 152, App
19	3080	94.5	586	4	US-10-117-982-152	Sequence 152, App
20	3080	94.5	586	4	US-10-313-986-152	Sequence 152, App
21	3080	94.5	586	5	US-10-775-972-152	Sequence 152, App
22	3080	94.5	586	5	US-10-922-124-152	Sequence 152, App
23	3080	94.5	586	5	US-10-623-155-152	Sequence 152, App
24	3066	94.0	586	4	US-10-716-359-22	Sequence 22, Appl
25	3066	94.0	586	6	US-11-109-831-22	Sequence 22, Appl
26	3033	93.0	641	4	US-10-716-359-13	Sequence 13, Appl
27	3033	93.0	641	5	US-10-469-469-310	Sequence 310, App
28	3033	93.0	641	6	US-11-109-831-13	Sequence 13, Appl
29	3029	92.9	641	3	US-09-735-705-339	Sequence 339, App
30	3029	92.9	641	3	US-09-850-716A-339	Sequence 339, App
31	3029	92.9	641	3	US-09-897-778-339	Sequence 339, App
32	3029	92.9	641	4	US-10-007-700-339	Sequence 339, App
33	3029	92.9	641	4	US-10-117-982-339	Sequence 339, App
34	3029	92.9	641	4	US-10-313-986-339	Sequence 339, App
35	3029	92.9	641	5	US-10-775-972-339	Sequence 339, App
36	3029	92.9	641	5	US-10-922-124-339	Sequence 339, App
37	3029	92.9	641	5	US-10-623-155-339	Sequence 339, App
38	3029	92.9	641	5	US-10-469-469-282	Sequence 282, App
39	3029	92.9	641	5	US-10-469-469-298	Sequence 298, App
40	3025	92.8	680	3	US-09-735-705-342	Sequence 342, App
41	3025	92.8	680	3	US-09-850-716A-342	Sequence 342, App
42	3025	92.8	680	3	US-09-897-778-342	Sequence 342, App
43	3025	92.8	680	4	US-10-007-700-342	Sequence 342, App
44	3025	92.8	680	4	US-10-117-982-342	Sequence 342, App
45	3025	92.8	680	4	US-10-313-986-342	Sequence 342, App

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 27, 2006, 20:35:01 ; Search time 13.7 Seconds
 (without alignments)
 3773.012 Million cell updates/sec

Title: US-10-716-359-4

Perfect score: 3260

Sequence: 1 atgttgtacctggaaaacaa.....tcaaagaggagggggagtga 1761

Scoring table: BLOSUM62

Xgapop	10.0	, Xgapext	0.5
Ygapop	10.0	, Ygapext	0.5
Fgapop	6.0	, Fgapext	7.0
Delop	6.0	, Delext	7.0

Searched: 390055 seqs, 97842647 residues

Total number of hits satisfying chosen parameters: 780110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10716359/runat_27122006_140426_732/app_query.fasta_1
-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=20000000000 -HOST=abss02p
-USER=US10716359@CGN_1_1_94@runat_27122006_140426_732 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Published_Applications_AA_New:*

1:	/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2:	/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3:	/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4:	/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5:	/EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6:	/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7:	/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8:	/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				
No.	Score	Match	Length	DB	ID
1	3033	93.0	641	7	US-11-340-715-4
Description					
Sequence 4, Appli					

2	2995	91.9	641	7	US-11-340-715-11	Sequence 11, Appli
3	1813	55.6	448	7	US-11-340-715-1	Sequence 1, Appli
4	1746	53.6	587	6	US-10-489-730-2	Sequence 2, Appli
5	1741	53.4	636	7	US-11-340-715-8	Sequence 8, Appli
6	1718.5	52.7	661	6	US-10-489-730-11	Sequence 11, Appli
7	1420.5	43.6	450	6	US-10-489-730-4	Sequence 4, Appli
8	1415.5	43.4	499	7	US-11-340-715-6	Sequence 6, Appli
9	1293.5	39.7	426	6	US-10-489-730-6	Sequence 6, Appli
10	1046	32.1	312	7	US-11-340-715-7	Sequence 7, Appli
11	960.5	29.5	349	7	US-11-340-715-9	Sequence 9, Appli
12	726	22.3	393	7	US-11-340-715-3	Sequence 3, Appli
13	726	22.3	393	7	US-11-009-357-6	Sequence 6, Appli
14	726	22.3	425	7	US-11-009-357-2	Sequence 2, Appli
15	721	22.1	393	6	US-10-546-829-1	Sequence 1, Appli
16	719	22.1	393	6	US-10-538-066-367	Sequence 367, App
17	719	22.1	393	7	US-11-315-777-9	Sequence 9, Appli
18	719	22.1	393	7	US-11-319-873-9	Sequence 9, Appli
19	719	22.1	393	7	US-11-254-926-9	Sequence 9, Appli
20	719	22.1	393	7	US-11-304-280-9	Sequence 9, Appli
21	719	22.1	393	7	US-11-239-548-9	Sequence 9, Appli
22	718	22.0	393	7	US-11-371-354-72585	Sequence 72585, A
23	714	21.9	393	7	US-11-404-146-3	Sequence 3, Appli
24	713	21.9	354	6	US-10-538-066-763	Sequence 763, App
25	316	9.7	102	6	US-10-538-066-765	Sequence 765, App
26	291.5	8.9	100	6	US-10-489-730-12	Sequence 12, Appli
27	285.5	8.8	100	6	US-10-489-730-14	Sequence 14, Appli
28	284.5	8.7	100	6	US-10-489-730-13	Sequence 13, Appli
29	163	5.0	2240	6	US-10-544-731-4	Sequence 4, Appli
30	163	5.0	2258	6	US-10-544-731-3	Sequence 3, Appli
31	163	5.0	2264	6	US-10-544-731-5	Sequence 5, Appli
32	154.5	4.7	634	7	US-11-293-697-3340	Sequence 3340, Ap
33	149.5	4.6	693	7	US-11-293-697-3849	Sequence 3849, Ap
34	143.5	4.4	1113	7	US-11-056-355B-77057	Sequence 77057, A
35	142.5	4.4	1690	6	US-10-516-780-28	Sequence 28, Appli
36	141	4.3	690	6	US-10-449-902-41507	Sequence 41507, A
37	140.5	4.3	312	6	US-10-953-349-31493	Sequence 31493, A
38	140.5	4.3	312	7	US-11-056-355B-68325	Sequence 68325, A
39	140	4.3	691	7	US-11-056-355B-79590	Sequence 79590, A
40	140	4.3	718	7	US-11-056-355B-79589	Sequence 79589, A
41	140	4.3	847	7	US-11-056-355B-79588	Sequence 79588, A
42	138.5	4.2	5178	6	US-10-700-439-178	Sequence 178, App
43	138.5	4.2	5179	6	US-10-541-749-151	Sequence 151, App
44	138.5	4.2	5179	7	US-11-105-233-185	Sequence 185, App
45	138	4.2	934	6	US-10-449-902-41077	Sequence 41077, A